



PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTGTTTCGTTT

MluI (558) **BspLU11I (566)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACGGCAGCGTCAACATGTTGCTCTGGGCTTGCCTTCTTGGTGC
1▶ M F A L G L P F L V L

Bsp120I (637) **Tth111I (688)**
601 CTTGGTGGCCTCGTTCGAGAGCCATCTGGGGTCTGGGGCCCAAGAACGTCCTCGAGAAAGACGCCGAGTTTGGCGCACCTACGTGGACGAGGTCAAC
11▶ L V A S V E S H L G V L G P K N V S Q K D A E F E R T Y V D E V N
701 AGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCCGCAACAGGACAGAGGGCGTGCCTGTGTCTGTAACGCTCTGAACAAGCAGAAGGGGG
45▶ S E L V N I Y T F N H T V T R N R T E G V R V S V N V L N K Q K G
801 CGCCGTTGCTGTTTGGTCCGCCAGAAGGAGCTGTGTCTCCAGGTGCCCTAATCTGCGAGGGATGTTTCAGCGCAAGTACCTTACCAAAA
78▶ A P L L F V V R Q K E A V V S F Q V P L I L R G M F Q R K Y L Y Q K
901 AGTGAACGAACCTGTGTGACCCCCACCAAGAATGAGTCGGAGATTCACTTCTTACGTGGATGTGCCACCCTGTCACCAGTCAACACCACATAC
111▶ V E R T L C Q P P T K N E S E I Q F F Y V D V S T L S P V N T T Y

ScaI (1082)
1001 CAGCTCCGGTCCAGCCGATGGACGATTTTGCTCAGGACTGGGAGCAGTTCACTTCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGT
145▶ Q L R V S R M D D F V L R T G E Q F S F N T T A A Q P Q Y F K Y E

StuI (1145)
1101 TCCTGAAGCGTGGACTCGGTAATGTCAAGTGACCTCCAACAAGGCCTTCCCTGCTCAGTCATCTCCATTCAAGGATGTGCTGTGCTGCTGTATGA
178▶ F P E G V D S V I V K V T S N K A F P C S V I S I Q D V L C P V Y D
1201 CCTGGACAACAACGTAGCCTTCCATCGGCATGTACCAGACGATACCAAGAAGCGCCATCACCGTACAGCGCAAAGACTTCCCAGCAACAGCTTTTAT
211▶ L D N N V A F I G M Y Q T M T K K A A I T V Q R K D F P S N S F Y

AgeI (1374)
1301 GTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGCTCCCTGCCTTTCTACCCCTTCGAGAAGATGAACCGGTGATCAAGGGCACCGCCAGA
245▶ V V V V V K T E D Q A C G G S L P F Y P F A E D E P V D Q G H R Q
1401 AAACCCTGTCAAGTGTGCTCAAGCAGTACGCTGTGAGGCATACGTCAGTGGGATGCTCTTTTGGCTGGGTATATTTCTCTCTTTTACCTGCTGAC
278▶ K T L S V L V S Q A V T S E A Y V S G M L F C L G I F L S F Y L L T

XhoI (1589)
1501 CGTCTCTGGCCTGCTGGGAGAACTGGAGGCAGAAGAAGACCCCTGCTGGTGGCCATTGACCGAGCCTGCCAGAAAGCGGTCAACCCTCGAGTCCTG
311▶ V L L A C W E N W R Q K K K T L L V A I D R A C P E S G H P R V L

Eco47III (1690)
1601 GCTGATTCTTTTCTGGCAGTTCCCTTATGAGGGTTACAACATATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCA
345▶ A D S F P G S S P Y E G Y N Y G S F E N V S G S T D G L V D S A G

XcmI (1769)
1701 CTGGGACCTCTCTTACGGTTACCAGGCCGCTCCTTTGAACCTGTAGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATGACTACGA
378▶ T G D L S Y G Y Q G R S F E P V G T R P R V D S M S S V E E D D Y D

ClaI (1813)
1801 CACATTGACCGACATCGATTCCGACAAGAATGTATTGACCAAGCAATACCTCTATGTGGCTGACCTGGCAGGAAGGACAAGCGTGTCTGCGGAAA
411▶ T L T D I D S D K N V I R T K Q Y L Y V A D L A R K D K R V L R K

PvuII (1963)
1901 AAGTACCAGATCTACTTCTGAAACATTGCCACCATGTGTCTTCTATGCCCTCCTGTGGTGCAGCTGGTATCACCTACCAGACGGTGGTGAATGTCA
445▶ K Y Q I Y F W N I A T I A V F Y A L P V V Q L V I T Y Q T V V N V
2001 CAGGGAATCAGGACATCTGCTACTACAACCTCTCTGCGCCACCCACTGGGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGTACATCCT
478▶ T G N Q D I C Y Y N F L C A H P L G N L S A F N N I L S N L G Y I L

FspI (2162)
Bsp120I (2153) **BamHI (2192)**
2101 GCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCAATGACCTCTGTGCCCTGGAATGTGGGATCCCC
511▶ L G L L F L L I I L Q R E I N H N R A L L R N D L C A L E C G I P

NcoI (2222)
2201 AAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGATGGAGGGGCTGCTCAGTCTGCTATCATGTGTGCCCAACTATACCAATTTCCAGT
545▶ K H F G L F Y A M G T A L M M E G L L S A C Y H V C P N Y T N F Q

BsrGI (2315) **SphI (2336)**
2301 TTGACACATCGTTTATGATGATGCGCGGACTCTGCATGCTGAAGCTTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCTACAGTGCCTACGC
578▶ F D T S F M Y M I A G L C M L K L Y Q K R H P D I N A S A Y S A Y A
2401 CTGCTGGCCATTGTCATCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTCTGGATCGTCTTCTCCATCATTCACATCATCGCC
611▶ C L A I V I F F S V L G V V F G K G N T A F W I V F S I I H I A

BbrPI (2575)

2501 ACCTGCTCCTCAGCACGCAGCTCTATTACATGGGCCGGTGGAACTGGACTCGGGGATCTTCCGCCGCATCTCCACGTGCTCTACACAGACTGCATCC
645▶ T L L L S T Q L Y Y M G R W K L D S G I F R R I L H V L Y T D C I
2601 GGCAGTGCAGCGGGCCGCTCTACGTGGACCGCATGGTCTGCTGGTCACTGGCAACGTCACTCACTGGTGCCTATGGGCTTATCATGGCCCC
678▶ R Q C S G P L Y V D R M V L L V M G N V I N W S L A A Y G L I M R P

BspEI (2780)

BspHI (2771)

2701 CAATGATTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCTTTACTTCGCCTTCTACATCATGAAGCTCCGGAGTGGGGAGAGGATC
711▶ N D F A S Y L L A I G I C N L L L Y F A F Y I I M K L R S G E R I

BstAPI (2819)

SapI (2853)

PstI (2897)

2801 AAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTTGGTCTGGGGCTTCGCGCTCTTCTTCTCCAGGGACTCAGCACCTGGCAGAAAACCCCTG
745▶ K L I P L L C I V C T S V V W G F A L F F F F Q G L S T W Q K T P
2901 CAGAGTCGAGGGAGCACAAACCGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATGTTGGGGTCTT
778▶ A E S R E H N R D C I L L D F F D D H D I W H F L S S I A M F G S F

NheI (3077)

3001 CCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGACGCGGACAAGATCTATGTCTTAGCAGGAGCTGGGCTAGCTGGCCAGACATGATAAG
811▶ L V L L T L D D D L D T V Q R D K I Y V F •
3101 ATACATTGATGAGTTTGGACAAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATA

HpaI (3215) MfeI (3226)

3201 AGCTGCAATAAACAGTTAACACAACAATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACA

EcoRI (3311)

3301 AATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCA

SapI (3493)

3401 TCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGTTTGAACAGTCTCTTC

SspI (3550)

SwaI (3564)

3501 ATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAATATTAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTT

3601 TTATTAGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGC

3701 AAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAA
141▶ N R T Y K L P I L E E I T T K V L K G N M E I L V F

BstXI (3854)

3801 AGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGAC
114▶ C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P H R V

StuI (3989)

3901 AGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCAGCAGACCAATGGCAATGGTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATG
81▶ A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I

4001 TGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTCTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCT
47▶ H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T A V E

XmnI (4131)

AseI (4197)

4101 CCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCTGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTATGCCGATGATT
14▶ V L E L D Q Q S I N F T K M

4201 AATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCCAT

SpeI (4352)

4301 TTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAA

SnaBI (4480)

4401 AATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAG

NdeI (4585)

4501 TAGGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCAATGACGTCAATAGGGGGCTACTTGGCATATGATACACTTG

4601 ATGTAAGTCCAAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATATTGAC

PaeI (4771)

PstI (4764)

SdaI (4763)

BspLU111 (4781)

4701 GTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAA

4801 GCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGG

4901 TGGCGAAACCCGACAGGACTATAAGATACCAGGCTTTCCCTGGAAGTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGT

ApaLI (5095)

5001 CCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCA
5101 CGAACCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACT
5201 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCT
5301 GCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCA
5401 GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTG

EagI (5531)

Pacl (5511) SwaI (5520) **NotI (5530)**

5501 GTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAAC
5601 ATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA